Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Title: Perfect score: Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters: Scoring table: Run on: OM nucleic - nucleic search, using sw model 4: 5: 7: 7: 7: 8: 9: 9: 110: 113: 114: 115: 118: 119: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 November 29, 2001, 04:04:14; Search time 6128.19 Seconds (without alignments) 2020.032 Million cell updates/sec 11351937 seqs, 5372889281 residues GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. gb_gss:*
em_gss_fun:*
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em_gss_lnv:*
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em_gss_pro:*
em_gss_vrt:*
em_gss_other:* em_htc:* em_estin:* gb_est1:*
gb_est2:*
gb_htc:* em_estov:* em_estro:* em_estba:* em_estpl:* em_estom: * em_esthum:* em_estfun:* 22703874

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB	Length	BB	ID	Description
c 1	664.4	57.7	674	10	AW978572	AW978572
c 2	606.6	52.7	657	10	AW370369	AW370369
ი 3	498.2	43.2	508	10	AA825207	AA825207
c 4	493	42.8	495	10	AW575965	AW575965
ი 5	454.4	39.4	456	10	AI379831	AI379831
ი 6	407	35.3	407	10	AI224367	AI224367
c 7	396.4	34.4	398	10	AW292092	AW292092
c 8	374.4	32.5	376	10	AI832007	AI832007
c 9	372.8	32.4	525	10	AI250843	AI250843
10	349.4	30.3	358	10	AW404913	AW404913
c 11	331.4	28.8	338	10	AA825205	AA825205
c 12	312.8	27.2	328	10	AW003249	AW003249

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																											16.4					
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11	10	10	11	10	11	11	H	10	10	10	10	10	10	10	10	11	10	10	10	11	10	11	10	10	13	10	10	13	10	13	10	10
BG759756	AW328037	AW732667	BI226934	BE295457	BI261356	BI225862	BI225045	BE513898	BE269500	BE268990	BE267967	BE398017	AW732980	AW500764	BE267581	BF128815	AW405686	AI391250	AW014278	BF605796	AW345961	BF082894	AA689513	AI468861	AQ518451	BE685287	AW480639	AQ572549	AW768336	AQ589625	AI250350	AI434322
BG759756 602711155	AW328037 dr03g06.x	AW732667 bb10h10.y	BI226934 602952063	BE295457 601174505	BI261356 602953358	BI225862 602950239	BI225045 602949269	BE513898 601316486	BE269500 601184704	BE268990 601184424	BE267967 601125372	BE398017 601290574	AW732980 bb18d04.y	AW500764 UI-HF-BNC	BE267581 601124363	BF128815 601811195	AW405686 UI-HF-BLC	AI391250 mb58c01.y	AW014278 UI-H-BIO-	BF605796 272392 MA	AW345961 26836 MAF	BF082894 QV1-BT082	AA689513 ns17q04.r	AI468861 ti43b01.x	AQ518451 HS_5101_F	BE685287 187456 MF	AW480639 32244 MAR					

ALIGNMENTS

BASE COUNT ORIGIN	source	FEATURES	Sec	Ema Pla	Fax	Tel	. 971	The	COMMENT Cor	JOURNAL Unp	met	TITLE ASS	Qua	,Ι.	AUTHORS Heg	REFERENCE 1	Мап	Euk	ORGANISM Hon	SOURCE hun	KEYWORDS EST.			DEFINITION EST	LOCUS AWS	AW978572/c	RESULT 1
/organism" Homo sapiens" /db_ref="taxon:9606" /clone_lib="MAGE resequences, MAGP" /note="Vector: pBluescriptsKm" 185 a 178 c 191 g 120 t	1674	Location/Qualifiers	Seq primer: Forward.	Email: johng@tigr.org Plate: 394	Fax: 301 838 0208		9712 Medical Center Dr., Rockville, MD 20850, USA	The Institute for Genomic Research	tact: John Quackenbush	Unpublished (2000)		Assessment of gene expression patterns in a model of colon tumor	Quackenbush, J.	,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and	Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt		Primates;	<pre>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</pre>	Homo sapiens	human.		AW978572.1 GI:8169840	AW978572	1 MAGE resequences, MAGP Homo sapiens cDNA	AW978572 674 bp mrna EST 02-JUN-2000		

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RESULT 2
AW370369/c
                                                                               COMMENT
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                                                                                               HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                             AW370369 657 bp mRNA EST 04-FEB-2000 RC1-BT0255-181099-012-f04 BT0255 Homo sapiens cDNA, mRNA sequence.
                        Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                           EST
  Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                         Contact: Simpson A.J.G
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                     Homo sapiens
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 Mismatches

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Pred. No. 1.1e-111;
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                                                                            ggcctgtgcttctgcttattcagtccttcagctcacggaagggatgctagtccgtgaagg 1084
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181099-012-f04&t3=1999-10-18&t4=1)
Seq.primer: puc 18 forward
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
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174 c 187 q 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="Adult"
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 Mismatches

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770 caccaggatgtgtgcccagccaggcctccagcacccccagtgcagctcgtgattggaaac 829
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                                                                                                                Local Similarity
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                                     500;
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AA825207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oc66e07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354692 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bonaido, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA825207.1 GI:2898504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 508)
                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                       constructed by Bento Soares and M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                          j. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pm713 vector. Library went through one round of normalization, and was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phote="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
/note="Ur---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:1354692"
/clone_lib="NCI_CGAP_GCB1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                      POLYA=Yes
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                                                                                                                                                                                                                                                                                                    primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cgapbs-r@mail.
                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:3059932"
                                                                                                                                                                                                                            /organism="Homo sapiens"
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1010 tggagggatgggtttggcctgtgcttctgcttattcagttccttcagctcacggaagggat 1069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 CACCAGGATGTGTGCCCAGCCAGGCCTCCAGCACCCCCAGTGCAGCTCGTGATTGGAAAC 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              890 tgtggacttggatgccctgtgggtatcagttctgctgacactttggcccgaaatagatcc 949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host="pH108 (LTI)"
/note="Vector: pT773-Pac; Site_1: Not1; Site_2: Eco RI;
/note="Vector: pT773-Pac; Site_1: Not1; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
                                                                                                                                                                                                                                                             /clone_lib="NIH_MGC_37"
/tlssue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
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                                                                                                                                                Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                          IMAGE Consortium (info@image.lln]
Insert Length: 746 Std Error: (
                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI379831.1 GI:4189684
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                                                                                                                           primer: -40UP from Gibco
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                                                                                                quality sequence stop: 455.
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                                                                         Location/Qualifiers
     /db_xref="taxon:9606"
                          /organism="Homo sapiens"
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    Mismatches

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Pred. No. 2.2e-80;
Trematches 2; Indels 0; Gaps
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                                                                                                                                                                                                                      KEYWORDS
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  JOURNAL
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                                                                         AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gagcctcagtgagcccatctgcacagtggggagcatggagggatgggtttggcctgtgct 1034
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                                                                                                                                                                                                                                                                                                          AI224367 407 bp mF
qx05f07.x1 NCI_CGAP_Lym12
Unpublished (1997)
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 407)
                            T'umor
                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                              AI224367.1 GI:3807080
                                                                                                                                                                                                                                                                      AI224367
                                                                                                                                                                                                                                                                                          mRNA sequence.
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                            Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a modified polylinker; Site_1: Not I; Site_2: Ecc RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified coNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-392087, 682632-687239,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     726408\hbox{-}728711, and 729096\hbox{-}731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE: 2087320"
/clone_lib="Soares_NFL_T_GBC_S1"
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99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1025 ggcctgtgcttctgcttattcagtccttcagctcacggaagggatgctagtccgtgaagg 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           965 atgtacaccggagcctcagtgagcccatctgcacagtggggagcatggagggatgggttt 1024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   347 CCAGCCAGGCCTCCAGCACCCCCAGTGCAGCTCGTGATTGGAAACTCACCATCGGCAGGC 288
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                                                                                                                                                                                                                                                             AW292092 398 bp mRNA EST 16-JAN-2000 UI-H-BIZ-agx-a-12-0-UI-H-SIDZ-AGX-a-12-0-UI-SIDZ-GGAP_SUb4 Homo sapiens cDNA clone IMAGE:2725559 3', mRNA sequence.
Unpublished (1997)
                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                      EST
                                                                                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 398)
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                        Homo sapiens
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Email: cgapbs-remail.nih.gov
unknown library type
Insert Length: 675 Std Error: 0
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                        Gene Index
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a 109 c 107 g 91 t
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/clone_lib="NCI_CGAP_Lym12"
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867 cattagagggagcccagtctggatgtggacttggatgccctgtgggtatcagttctgctg 926
                                                                                                                                                      source
                                                                                                                  398 CACTCCCAAATCCCCTTCATACCCACCAGGATGTGTGCCCCAGCCCAGGCCTCCAGCACCCC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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/note="Pwector: p773D-pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NCI_CGAP_Sub4 library is a subtracted library derived from the NCI_CGAP_Sub1 library which is a subtracted library derived from the NCI_CGAP_Sub1 library.

derived from the NCI_CGAP_Sub1 library, which is a subtracted library derived from the NCI_CGAP_Sub1 library, which is a subtracted library derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI_CGAP_FRAME.

NCI_CGAP_CO10, NCI_CGAP_CO16, NCI_CGAP_KIG11, NCI_CGAP_KIG12, NCI_CGAP_KIG13, NCI_CGAP_KIG11, NCI_CGAP_LO18, NCI_CGAP_KIG11, NCI_CGAP_LO18, NCI_CGAP_LO18, NCI_CGAP_LO18, NCI_CGAP_LO19, NCI_C
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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TAG_SEQ=CAAC"
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TAG_LIB-NCI_CGAP_Lu5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
813 agctcgtgattggaaactcaccatcggcaggcagtggttcggttttaagagagtggcattag 872
                                                                753 caaatccccttcatacccaccaggatgtgtgcccaggccaggcctccagcaccccccagtgc 812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  987 gcccatctgcacagtggggagcatggagggatgggttttggcctgtgcttctgcttattca 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 ACACTTTGGCCCGAAATAGATCCAGTGCTGAGCAAGCAATGTACACCGGAGCCTCAGTGA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             278 CATTACAGGGAGCCCAGTCTGGATGTGGACTTGGATGCCCTGTGGGTATCAGTTCTGCTG 219
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                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 375.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. CONSOTTIUM/LINI at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                     /note-"Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
sall; Site_2: Not1; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
a 105 c 97 g 82 t
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/clone_lib="NCI_CGAP_Lym12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="lymphoma, follicular mixed small and large
                                                                                                                                                                   32.5%; Score 374.4; DB 10; Length 376; 99.7%; Pred. No. 9.7e-59;
                                                                                                                                                 0; Mismatches
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Query Match
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                                                                                    377 CAAAATCCCCTTCATACCCACCAGNATGTGTGCCCAGCCAGGCCTCCAGCACCCCCAAGTG 318
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                                                                                                                  16 TTATTGCTCACTGTCA 1
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                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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AI250843
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Location/Qualifiers
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Insert Length: 1149
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National Cancer Institute, Cancer Genome Anai
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                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                              /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

a 141 c 136 g 104 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="lymphoma, follicular mixed small and large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NCI_CGAP_Lym12"
                                                                                                                                                                                                                         32.4%; Score 372.8; DB 10; Length 525; 99.2%; Pred. No. 1.7e-58;
                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Std Error: 0.00
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                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                       0; Gaps
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BASE COUNT
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                                                                      Query Match
          Matches 350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            932 ttggcccgaaatagatccagtgctgagcaatgtacaccggagcctcagtgagccca 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       872 gagggagcccagtctggatgtggacttggatgccctgtgggtatcagttctgctgacact 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 CAGCTCGTGATTGGAAACTCACCATCGGCAGGCAGTGGTTCGGTTTAAGAGATGGCATTA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 TTTATTGCTCACTGTCA 1
                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tctgcacagtggggagcatggggtttggcctgtgcttctgcttattcagtcct 1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGGCCCGAAATAGATCCAGTGCTGAGCAAGCAATGTACACCGGAGCCTCAGTGAGCCCA 138
                                   h 30.3%;
Similarity 99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW404913 358 bp mRNA EST 16-FEB-2000 UI-HF-BLO-acn-h-03-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059932 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 358)
                                                                                                                                                                                                    71 a
       Conservative
                                                                                                                                                                           /lab_nost="DHIOB (LTI)"
/lab_nost="DHIOB (LTI)"
/note="Vector: pTTT3-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pTTT3-Pac; Site_1: NotI; Site_1: NotI; Site_1: Eco RI;
/note="Vector: pTTT3-Pac; Site_1: NotI; Site_1: NotI; Site_1: Eco RI;
/note="Vector: pTT3-Pac; Site_1: NotI; Site_1: NotI; Site_1: Eco RI;
/note="Vector: pTT3-Pac; Site_1: NotI; Site_1: NotI; Site_1: Eco RI;
/note="Vector: pTT3-Pac; Site_1: NotI; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NIH_MGC_37"
/tissue_type="lymph"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3059932"
                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_line="MGC85"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="germinal center B cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
       0
                               Score 349.4; DB 1
Pred. No. 3.5e-54;
       Mismatches
                                                        DB 10; Length 358;
   1;
   Indels
   0;
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA825205.1 GI:2898502
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                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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308 TCCAGTTTCTGGGAAATATCAGACCATGGCCAGATTGACTCTATGGAGCAG 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 ttctcccagctgcccgccgtgtggccagctctaccccgggaggaagtaccgagcagcggat 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 GTGCACTTGTGGCAGATGGCAGTGCATACCCGGGAGCTACTCTCCTCCGGCCAGATGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 gtgcacttgtggcagatggcagtgcatacccgggagctactctcctccggccagatgccc 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 ccctcgcgtagggaatgggccagggcctcccagggcagcagatatgaacccagcatcaca 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 TTCTCCCAGCTGCCCGCCGTGTGGCAGCTCTACCCCGGGAGGAAGTACCGAGCAGCGGAT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 CCCTCGCGTAGGGAATGGGCCAGGGCCTCCCAGGGCAGCAGATATGAACCCAGCATCACA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88 cctggcatctacgaagatgaggaggggagaacctgggtgactgtggtcgtgcgtfcaat 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 atggcctccgaagcttctgtgcgtctaggggtgccccttggccgtctgtggatccagagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 CCTGGCATCTACGAAGATGAGGAGGGGAGAACCTGGGTGACTGTGGTCGTGCGGTTCAAT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 ATGGCCTCCGAAGCTTCTGTGCGTCTAGGGGTGCCCCCTGGCCGTCTGTGGATCCAGAGG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1077 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oc66e05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354688 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               quality sequence stop: 135.
/tissue_type="germinal center B cell"
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                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_GCB1"
                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:1354688"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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AW003249/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1000 gtggggagcatggagggatgggtttggcctgtgcttctgcttattcagtccttcagctca 1059
                                                                                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 GTGGGGAGCATGGGATGGGTTTGGCCTGTGCTTCTGCTTATTCAGTCCTTCAGCTCA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                940 aaatagatccagtgctgagcaagcaatgtacaccggagcctcagtgagcccatctgcaca 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     880 ccagtctggatgtggacttggatgccctgtgggtatcagttctgctgacactttggcccg 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338 GATTGGAAACTCACCATCGGCAGGCAGTGGTTCGGTTTAAGAGATGGCATTACAGGGAGC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 AAATAGATCCAGTGCTGAGCAAGCAATGTACACCGGAGCCTCAGTGAGCCCATCTGCACA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 CCAGTCTGGATGTGGACTTGGATGCCCTGTGGGTATCAGTTCTGCTGACACTTTGGCCCG 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW003249
                                                                                                                                                                                                                              CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                      Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 328)
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/clone="IMAGE:2476070"
/clone_lib="NCI_CGAP_GC6"
                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                          Location/Qualifiers
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                                                                                                                                                      -40UP from Gibco
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h: 384 Std Error: 0.00
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 AGCCCATCTGCACAGTGGGGGAGCATGGAGGGATGGGTTTTGGCCTTGTTCTTGCTTATTC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   986 agcccatctgcacagtggggagcatggagtgtgggtttggcctgtgcttcttgcttattc 1045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 TTAAACTTTATTGCTCACTGTCAAAAAA 1
                                                             Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1751 Std Error: 0.00
Seq.primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 315)
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                    High quality sequence stop: 308.
Location/Qualifiers
                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                   Unpublished (1997)
                                                                                                                                                                                                                                                                                                          Tumor Gene Index
                                                                                                                                                                                                                                                                                                                              National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. " a 95 c 73 g 76 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 TTGGCCCGAAATAGATCCAGTGCTGAGCAAGCAATGTACACCGGAGCCTCAGTGAGCCCA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            932 ttggcccgaaatagatccagtgctgagcaatgtacaccggagcctcagtgagccca 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          872 gagggagcccagtctggatgtggacttggatgcctqtgggtatcagttctgctgacact 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 GAGGGAGCCCAGTCTGGATGTGGACTTGGATGCCCTGTGGGTATCAGTTCTGCTGACACT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 TTTATTGCTCACTGTC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                               High quality sequence stop: 269.
                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALZS0350 300 bp mRNA EST 21-DEC-1998 qx04c01.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2000352 3',
                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                              National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                 1. .300
/clone_lib="NCI_CGAP_Lym12"
                   /clone="IMAGE: 2000352"
                                                                                              Location/Qualifiers
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Sall; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
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/clone_lib="NCI_CGAP_Lym12"
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99.78;
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                                                                                                                                                      Std Error: 0.00
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                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1025 ggcctgtgcttctgcttattcagtccttcagctcagctaagggaatggatgctagtccgtgaagg 1084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 AGTGGTTCGGTTTAAGAGATGGCATTAGAGGGAGCCCAGTCTGGATGTGGACTTGGATGC 241
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                                                    High quality sequence stop: 492.
Location/Qualifiers
                                                                                                                                                Tel: (206) 616-3618
Fax: (206) 616-3818
Email: jwallace@u_washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                               High Throughput Sequencing Center University of Washington
                                                                                                   Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                          scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                           401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                     99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 492)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ589625 492 bp DNA GSS 08-JUN-1999 HS_2132_A1_D12_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens_genomic clone Plate=2132 Col=23 Row=G, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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               /organism="Homo sapiens"
/db_xref="taxon:9606"
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99.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 TCCCATGGCAGCACATATGAACCTAGCATCACAGTGCACATGTGGTAGATGCCAGTGCAC 183
                                                                       387 NCTCAGTGAGGATCTTTGTGTACTTGCTATTCCCGTTGCACACCCCAGCGTGGCCTTCTTG 446
                                                                                           475 cetcagtgaggatetteatgtaeetgetettetgtttgeaeaeceageatageeteettg 534
                                                                                                                                               358 -----CTCCTCTGGCCTCATGTCTCTCTGGCCC 386
                                                                                                                                                                             300 --CCAGATCGTCTCCATGGAGCAGCTGGTCCTAACATATTGGCCGGCAAGGAATAACTGA 357
                                                                                                                                                                                                                                       355 ggccagattgactctatggagcagctggtcctaacatatcagccggagaggaaagactga 414
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a 148 c 124 g 112 t 5 others
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
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Search completed: November 29, 2001, 05:49:45 Job time: 6331 sec